II.   AMENDMENTS TO THE CLAIMS

Please amend the claims as follows:

1.   (Previously Presented) A system for dynamically implementing a chain of Web services from a client on the World Wide Web to execute a workflow for analyzing microarray data, comprising:

a database for storing a list of available Web services, wherein each listed Web service includes a description of a task performed by the Web service and an input signature and an output signature of the Web service, wherein the Web service comprises a computer program accessible over the World Wide Web; and

a selecting system for forming the chain of Web services by selecting a Web service from the list of available Web services for each of a plurality of tasks in the workflow, wherein the workflow comprises a series of linked tasks and a specified input and output format, wherein the selecting system dynamically matches the input signature of a first Web service with the specified input of the workflow and the output signature of the first Web service with the input signature of an adjacent Web service and the output signature of a second Web service with the specified output format to ensure that each selected Web service is compatible with the adjacent Web service in the chain of Web services and the specified input and output formats.

2.   (Original) The system of claim 1, wherein the workflow comprises a microarray analysis workflow.

3. (Original) The system of claim 1, further comprising a workflow generator for creating the workflow.

4. (Original) The system of claim 1, wherein the list of available Web services resides locally with the client.

5. (Original) The system of claim 1, further comprising a system for collecting and storing available Web services data.

6. (Original) The system of claim 1, further comprising a system for inputting sequence data into the workflow execution.

7. (Previously Presented) The system of claim 1, wherein the input signature comprises a FASTA XML format for a set of input sequences and the output signature comprises an XML file format for providing spatial microarray placement data.

8.   (Previously Presented) A program product, stored on a recordable medium for executing a workflow for analyzing microarray data by dynamically implementing Web services from a client on the World Wide Web, comprising:

means for storing a list of available Web services, wherein each listed Web service includes a description of a task performed by the Web service, and an input signature and an output signature of the Web service; and

means for forming a chain of Web services by selecting a Web service from the list of available Web services for each of a plurality of tasks in the workflow, wherein the workflow comprises a series of linked tasks and a specified input and output format, wherein the forming means dynamically matches the input signature of a first Web service with the specified input format and the output signature of the first Web service with the input signature of an adjacent Web service and the output signature of a second Web service with the specified output format to ensure that each selected Web service is compatible with the adjacent Web service in the chain of Web services and the specified input and output formats.

9.   (Original) The program product of claim 8, wherein the workflow comprises a microarray analysis workflow.

10.   (Original) The program product of claim 8, wherein the workflow comprises a bioinformatics workflow.

11. (Original) The program product of claim 8, further comprising means for creating the workflow.

12. (Original) The program product of claim 8, wherein the storage means resides locally with the client.

13. (Original) The program product of claim 12, further comprising means for collecting and storing available Web services data in said storage means.

14. (Original) The program product of claim 8, further comprising a system for inputting sequence data into the workflow execution.

15. (Previously Presented) The program product of claim 8, wherein the input signature comprises a FASTA XML format for a set of input sequences and the output signature comprises an XML file format for providing spatial microarray placement data.

16. (Previously Presented) A method for executing a bioinformatics workflow from a client on the World Wide Web, comprising:

providing a workflow having a plurality of linked tasks and a specified input and output format;

providing a list of known bioinformatics Web services, wherein each listed Web service includes a description of a task performed by the Web service, and an input signature and an output signature of the Web service, further wherein the Web service comprises a computer program accessible over the World Wide Web;

selecting a Web service from the list of known bioinformatics Web services for each task in the bioinformatics workflow to form a chain of Web services, wherein the selecting step dynamically matches the input signature of a first Web service with the specified input of the workflow and the output signature of the first Web service with the input signature of an adjacent Web service and the output signature of a second Web service with the specified output format to ensure that each selected Web service is compatible with the adjacent Web service in the chain of Web services and that the input and output signatures are compatible with the specified input and output; and

calling each selected Web service in the chain to execute the bioinformatics workflow.

17. (Original) The method of claim 16, wherein the bioinformatics workflow comprises a microarray analysis.

18.   (Original) The method of claim 16, wherein the list of known bioinformatics Web services resides locally to the client.

19.   (Previously Presented) The method of claim 16, wherein the input signature comprises a FASTA XML format for a set of input sequences and the output signature comprises an XML file format for providing spatial microarray placement data.

20.   (Original) The method of claim 19, wherein the step of calling each selected Web service includes the step of providing a set bioinformatics data to a first Web service in the chain in the specified input format.